

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 03:08:07 ; Search time 234 Seconds
(without alignments)
1761.178 Million cell updates/sec

Title: US-09-660-568-49

Perfect score: 183
Sequence: 1 cacacactccccattctga.....ctgtctctcggagctcaacca 183

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
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- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	183	100.0	183	19	AAV38517
2	183	100.0	183	20	AAZ30719
3	41	22.4	2113	23	AA577249
4	35.2	19.2	164	22	ABA51400
5	35.2	19.2	164	22	ABA69411
6	35.2	19.2	164	22	ABA36346
7	35.2	19.2	164	22	AAK17679
8	35.2	19.2	164	22	AAK43494
9	35.2	19.2	164	22	AAI24280

10	33.6	18.4	1524	23	ABL30203	Drosophila melanog
11	32.8	17.9	3819	23	ABL30202	Drosophila melanog
12	31.2	17.0	3698	22	AAK73760	Human immune/haema
13	31.2	17.0	3698	22	AAK83893	Human immune/haema
14	31.2	17.0	10548	22	AAK64703	Human immune/haema
15	31.2	17.0	10548	22	AAK69813	Human immune/haema
16	31.2	17.0	10548	22	AAK73759	Human immune/haema
17	31.2	17.0	10548	22	AAK80461	Human immune/haema
18	31.2	17.0	10548	22	AAK83894	Human immune/haema
19	30.8	16.8	5616	22	AAK79614	Human immune/haema
20	30.6	16.7	3387	23	AA591234	DNA encoding novel
21	30.6	16.7	5216	22	AA528261	Genomic sequence #
22	30.6	16.7	5216	22	AA531528	Human DNA for a no
23	30.6	16.7	5216	24	ABQ66852	Human polynucleoti
24	30.2	16.5	433	22	AA189606	Human polynucleoti
25	29.8	16.3	13852	22	ABA17744	Human nervous syst
26	29.8	16.3	13852	22	ABA17745	Human nervous syst
27	29.8	16.3	13852	22	ABA21395	Human nervous syst
28	29.8	16.3	13852	22	ABA21396	Human nervous syst
29	29.6	16.2	4068	22	AA186707	Human polynucleoti
30	29.2	16.0	2086	23	ABL12837	Drosophila melanog
31	29.2	16.0	3598	22	AA164774	Human glucose tran
32	29.2	16.0	18733	22	AAK80682	Human immune/haema
33	29.2	16.0	100301	24	ABQ88176	Human osteoblast d
34	29	15.8	3212	24	ABK11142	CDNA of human clon
35	29	15.8	38886	20	AA223897	Murine LOBO homolo
36	29	15.8	49999	20	AA223891	Murine LOBO homolo
37	28.8	15.7	431	21	AA283887	Human secreted pro
38	28.8	15.7	1090	18	AA72790	Metastasis inducin
39	28.8	15.7	8894	23	ABK42719	Genomic sequence #
40	28.4	15.5	1089	24	ABK63947	CDNA encoding huma
41	28.4	15.5	2001	24	AA516204	Human disulfide co
42	28.4	15.5	2513	24	AA516206	Human disulfide co
43	28.4	15.5	44576	21	AA261522	Cosmid CVQ14 conta
44	28.2	15.4	341	22	ABA16249	Human nervous syst
45	28.2	15.4	1907	20	AAV84508	Human secreted pro

ALIGNMENTS

RESULT 1

AAV38517 standard; DNA; 183 BP.

AAV38517;

08-OCT-1998 (first entry)

DNA marker of metastatic prostate cancer, UC Band#321.

DNA marker; metastatic prostate cancer; human; UC Band#321; detection;

disease marker identification; lupus erythematosus; rheumatoid arthritis;

multiple sclerosis; asthma; myasthenia gravis; autoimmune thyroiditis;

amyloid lateral sclerosis; interstitial cystitis; prostatitis; ss.

Homo sapiens.

WO9824935-A1.

11-JUN-1998.

05-DEC-1997; 97WO-US22105.

24-MAR-1997; 97US-0041576.

06-DEC-1996; 96US-0032619.

12-DEC-1996; 96US-0032701.

(UROC-) UROCOR INC.

An G, O'Hara M, Ralph D, Veltri R;

WPI; 1998-333350/29.

XX Identifying markers for disease states - by amplifying RNA from
 PT peripheral blood and identifying RNA which is differential expressed
 PT between normal and disease state subjects
 XX
 PS Claim 17; Page 92; 158pp; English.
 XX
 CC This sequence represents a DNA marker of metastatic prostate cancer,
 CC designated UC Band#321, and was identified using a method of the
 CC invention. The method is for identifying markers for a disease state, and
 CC comprises: (a) providing a first set of peripheral blood mRNAs from one
 CC or more subjects known to exhibit the disease state and a second set of
 CC peripheral blood mRNAs from one or more normal subjects; (b) amplifying
 CC both sets of mRNAs to provide nucleic acid amplification products;
 CC (c) comparing the sets of amplification products; and (d) identifying
 CC those mRNAs that are differentially expressed between normal subjects and
 CC subjects exhibiting the disease state; where a difference in quantity of
 CC expression of an mRNA is indicative of a disease marker. This marker
 CC sequence can be used in a method of detecting a metastatic cancer disease
 CC state, especially for detection prostate cancer. Using the methods, a
 CC disease state may be detected, diagnosed, or a prognosis may be delivered
 CC by examining a blood sample rather than relying on a more invasive, or
 CC less sensitive test. In addition, a subject may be monitored for disease
 CC progression, status and response to therapies through monitoring of
 CC differentially expressed disease markers. The methods can be used for
 CC diseases such as cancer (especially metastatic or prostate cancer),
 CC asthma, lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
 CC myasthenia gravis, autoimmune thyroiditis, amyloid lateral sclerosis,
 CC interstitial cystitis, prostatitis or other systemic or chronic conditions.
 XX
 SQ Sequence 183 BP; 43 A; 52 C; 45 G; 43 T; 0 other;
 Query Match 100.0%; Score 183; DB 19; Length 183;
 Best Local Similarity 100.0%; Pred. No. 2.8e-53;
 Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CACACACTCCCCATCTGAGGCCCAAGAGGCTCATCCCTAAGGATGCCAGAGATCCAA 60
 DB 1 CACACACTCCCCATCTGAGGCCCAAGAGGCTCATCCCTAAGGATGCCAGAGATCCAA 60
 QY 61 GTGCAGAGGAGAAATGTGGTGGGCTATTATTATCCCCAGTGCCTTCCCTGGGCTAT 120
 DB 61 GTGCAGAGGAGAAATGTGGTGGGCTATTATTATCCCCAGTGCCTTCCCTGGGCTAT 120
 QY 121 GGATGAACAGTGGCTGACATTCATCTAGGAAGAGCTATGGCTTCTGCTCTCGGAGCTCA 180
 DB 121 GGATGAACAGTGGCTGACATTCATCTAGGAAGAGCTATGGCTTCTGCTCTCGGAGCTCA 180
 181 CCA 183
 181 CCA 183
 RESULT 2
 AAZ30719
 ID AAZ30719 standard; cDNA; 183 BP.
 XX
 AC AAZ30719;
 XX
 DT 19-JAN-2000 (first entry)
 XX
 XX Human UC Band #321 cDNA.
 XX
 KW UC Band #321; marker; expression; diagnosis;
 KW differential; disease; cancer; metastatic; breast cancer; prostate;
 KW peripheral leukocyte; immune response; asthma; lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis;
 KW autoimmune thyroiditis; amyotrophic lateral sclerosis; ALS;
 KW interstitial cystitis; prostatitis; mRNA; reverse transcriptase PCR;
 KW RT-PCR; screening; early; diagnosis; prognosis; monitoring; ss.
 XX
 OS Homo sapiens.
 XX

PN WO9949083-A1.
 XX
 PD 30-SEP-1999.
 XX
 PF 24-MAR-1999; 99WO-US06488.
 XX
 PR 24-MAR-1998; 98US-0046894.
 XX
 PA (UROC-) UROCOR INC.
 XX
 PI Ralph D, An G, O'Hara SM, Veltri RW;
 XX
 DR WPI; 1999-591105/50.
 XX
 PT Identifying markers of human disease, specifically for diagnosis of
 PT metastatic prostatic and breast cancers
 XX
 PS Claim 17; Page 124-125; 225pp; English.
 XX
 CC This sequence represents a human cDNA sequence designated UC Band #321,
 CC which encodes a previously undescribed gene product. The expression of
 CC this gene in peripheral leukocytes was examined using reverse
 CC transcriptase-PCR (RT-PCR) primers AAZ30739-230740. This gene was found
 CC to be differentially expressed between healthy subjects and patients
 CC with metastatic cancers (especially those of the prostate or breast) and
 CC may therefore be used as a marker for such diseases. Detecting
 CC levels of such human disease markers is used for diagnosis (also
 CC prognosis and monitoring) of diseases, including metastatic or
 CC organ-confined cancers, and diseases which also elicit an immune
 CC response such as asthma, lupus erythematosus, rheumatoid arthritis,
 CC multiple sclerosis, myasthenia gravis, autoimmune thyroiditis,
 CC amyotrophic lateral sclerosis (ALS), interstitial cystitis, and
 CC prostatitis, but especially metastatic prostatic and breast cancer. A
 CC particular use is differentiating between prostatic cancer and benign
 CC prostatic hypertrophy, and between advanced and localised prostatic
 CC cancer. By multivariate analysis of several different markers. Cancers
 CC can be treated by administering sequences antisense to sequences that
 CC encode human disease markers. This method detects a leukocyte response
 CC to disease rather than products of diseased cells, so is suitable for
 CC large-scale screening of asymptomatic subjects. Disease can be detected
 CC at an early stage, when few, if any, diseased cells are present in the
 CC circulation. Analysis of blood samples eliminates the need for more
 CC invasive methods for obtaining samples.
 XX
 SQ Sequence 183 BP; 43 A; 52 C; 45 G; 43 T; 0 other;
 Query Match 100.0%; Score 183; DB 20; Length 183;
 Best Local Similarity 100.0%; Pred. No. 2.8e-53;
 Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CACACACTCCCCATCTGAGGCCCAAGAGGCTCATCCCTAAGGATGCCAGAGATCCAA 60
 DB 1 CACACACTCCCCATCTGAGGCCCAAGAGGCTCATCCCTAAGGATGCCAGAGATCCAA 60
 QY 61 GTGCAGAGGAGAAATGTGGTGGGCTATTATTATCCCCAGTGCCTTCCCTGGGCTAT 120
 DB 61 GTGCAGAGGAGAAATGTGGTGGGCTATTATTATCCCCAGTGCCTTCCCTGGGCTAT 120
 QY 121 GGATGAACAGTGGCTGACATTCATCTAGGAAGAGCTATGGCTTCTGCTCTCGGAGCTCA 180
 DB 121 GGATGAACAGTGGCTGACATTCATCTAGGAAGAGCTATGGCTTCTGCTCTCGGAGCTCA 180
 181 CCA 183
 181 CCA 183
 RESULT 3
 AAZ307249
 ID AAZ307249 standard; cDNA; 2113 BP.
 XX
 AC AAZ307249;
 XX

RESULT 5

ABA69411
ID ABA69411 standard; DNA; 164 BP.
XX AC
XX ABA69411;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #17716.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200157277-A2.
PN
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
XX Claim 4; SEQ ID NO 17716; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
XX
XX Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 164 BP; 39 A; 39 C; 44 G; 42 T; 0 other;
Query Match 19.2%; Score 35.2; DB 22; Length 164;
Best Local Similarity 71.9%; Pred. No. 0.031;
Matches 46; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 52 GAGATCAAGTGCAGAGAGAGATGTGGTGGAGCTATTATTCCTCCAGTGCCTTCCCTG 111
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 100 GAGATCAGAGCAGCAGAGAGAGATGAAGTCAGGATATTTATTCCTTGGCTCTCTCTTG 159
QY 112 CTGG 115
DB 160 TGGG 163
RESULT 6
ABA36346
ID ABA36346 standard; DNA; 164 BP.
XX AC
XX ABA36346;
XX
DT 23-JAN-2002 (first entry)

XX

DE Probe #14812 for gene expression analysis in human heart cell sample.

XX

KW Human; gene expression; heart; microarray; vascular system; probe;

KW

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW

KW congenital heart disease; ss.

XX

OS Homo sapiens.

XX

XX WO200157274-A2.

PN

XX 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US00666.

XX

XX 04-FEB-2000; 2000US-0180312.

PR

PR 26-MAY-2000; 2000US-0207456.

PR

PR 30-JUN-2000; 2000US-0608408.

PR

PR 03-AUG-2000; 2000US-0632366.

PR

PR 21-SEP-2000; 2000US-0234687.

PR

PR 27-SEP-2000; 2000US-0236359.

PR

PR 04-OCT-2000; 2000GB-0024263.

XX

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA

XX Penn SG, Hanzel DK, Chen W, Rank DR;

PI

XX WPI; 2001-483447/52.

XX

XX Human genome-derived single exon nucleic acid probes useful for

PT

PT analyzing gene expression in human fetal liver -

XX

XX Claim 4; SEQ ID NO 17716; 639pp + sequence listing; English.

XX

XX The invention relates to a single exon nucleic acid probe for

CC

CC measuring human gene expression in a sample derived from human foetal

CC

CC liver. The single exon nucleic acid probes may be used for predicting,

CC

CC measuring and displaying gene expression in samples derived from human

CC

CC fetal liver. The present sequence is a single exon nucleic acid

CC

CC probe of the invention.

XX

XX Note: The sequence data for this patent did not form part of the

CC

CC printed specification, but was obtained in electronic format directly

CC

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 164 BP; 39 A; 39 C; 44 G; 42 T; 0 other;

XX

Query Match 19.2%; Score 35.2; DB 22; Length 164;

XX

Best Local Similarity 71.9%; Pred. No. 0.031;

XX

Matches 46; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY

QY 52 GAGATCAAGTGCAGAGAGAGATGTGGTGGAGCTATTATTCCTCCAGTGCCTTCCCTG 111

DB

DB 100 GAGATCAGAGCAGCAGAGAGAGATGAAGTCAGGATATTTATTCCTTGGCTCTCTCTTG 159

QY

QY 112 CTGG 115

DB

DB 160 TGGG 163

RESULT 7

AAK17679

ID

ID AAK17679 standard; DNA; 164 BP.

XX

XX AAK17679;

AC

XX 05-NOV-2001 (first entry)

DT

XX Human brain expressed single exon probe SEQ ID NO: 17670.

DE

XX Human; brain expressed exon; gene expression analysis; probe;

KW

```
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX Homo sapiens.
XX WO200157275-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00667.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX Example 4; SEQ ID NO: 17670; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX SQ Sequence 164 BP; 39 A; 39 C; 44 G; 42 T; 0 other;
XX Query Match 19.2%; Score 35.2; DB 22; Length 164;
XX Best Local Similarity 71.9%; Pred. No. 0.031;
XX Matches 46; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Oy 52 GAGATCCAGTGCGAGAGAGAGATGTGTGAGGCTATTATTTCCCGAGTCCCTTCCCTG 111
Db 100 GAGATCAGAGAGAGAGAGAGATGTGTGAGGCTATTATTTCCCGTGGCTCTCTCTTG 159
Oy 112 CTGG 115
Db 160 TGGG 163
XX RESULT 8
XX AAK43494
XX ID AAK43494 standard; DNA; 164 BP.
XX AC AAK43494;
XX 06-NOV-2001 (first entry)
XX Human bone marrow expressed single exon probe SEQ ID NO: 18051.
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX Homo sapiens.
XX WO200157276-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00668.
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX Homo sapiens.
XX WO200157275-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00667.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX Example 4; SEQ ID NO: 17670; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX SQ Sequence 164 BP; 39 A; 39 C; 44 G; 42 T; 0 other;
XX Query Match 19.2%; Score 35.2; DB 22; Length 164;
XX Best Local Similarity 71.9%; Pred. No. 0.031;
XX Matches 46; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Oy 52 GAGATCCAGTGCGAGAGAGAGATGTGTGAGGCTATTATTTCCCGAGTCCCTTCCCTG 111
Db 100 GAGATCAGAGAGAGAGAGAGATGTGTGAGGCTATTATTTCCCGTGGCTCTCTCTTG 159
Oy 112 CTGG 115
Db 160 TGGG 163
XX RESULT 8
XX AAK43494
XX ID AAK43494 standard; DNA; 164 BP.
XX AC AAK43494;
XX 06-NOV-2001 (first entry)
XX Human bone marrow expressed single exon probe SEQ ID NO: 18051.
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX Homo sapiens.
XX WO200157276-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00668.
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XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -
XX Example 4; SEQ ID NO: 18051; 658pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX the probes of the invention.
XX SQ Sequence 164 BP; 39 A; 39 C; 44 G; 42 T; 0 other;
XX Query Match 19.2%; Score 35.2; DB 22; Length 164;
XX Best Local Similarity 71.9%; Pred. No. 0.031;
XX Matches 46; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Oy 52 GAGATCCAGTGCGAGAGAGAGATGTGTGAGGCTATTATTTCCCGAGTCCCTTCCCTG 111
Db 100 GAGATCAGAGAGAGAGAGAGATGTGTGAGGCTATTATTTCCCGTGGCTCTCTCTTG 159
Oy 112 CTGG 115
Db 160 TGGG 163
XX RESULT 9
XX AAI24280
XX ID AAI24280 standard; DNA; 164 BP.
XX AC AAI24280;
XX 12-OCT-2001 (first entry)
XX Probe #14213 for gene expression analysis in human cervical cell sample.
XX Probe: human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer; ss.
XX Homo sapiens.
XX WO200157278-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00670.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA
```

PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
PS Claim 25; SEQ ID No 14213; 487pp; English.
XX The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human Hela cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 164 BP; 39 A; 39 C; 44 G; 42 T; 0 other;
Query Match 19.2%; Score 35.2; DB 22; Length 164;
Best Local Similarity 71.9%; Pred. No. 0.031;
Matches 46; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 52 GAGATCCAAAGTCGACGAGAGAGATGGTGAGGCTATTATTCCCGCTTCCCTG 111
DB 100 GAGTCAGAGCAGCAGAAAGAGAGATGAAGTGAGGATATTATTCCTGCTCTCTCTG 159
QY 112 CTGG 115
DB 160 TGGG 163
RESULT 10
ABL30203
ID ABL30203 standard; DNA; 1524 BP.
XX ABL30203;
AC ABL30203;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 42082.
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX Drosophila melanogaster.
XX WO200171042-A2.
PN 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX Claim 1; SEQ ID NO 42082; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 1524 BP; 455 A; 333 C; 353 G; 383 T; 0 other;
Query Match 18.4%; Score 33.6; DB 23; Length 1524;
Best Local Similarity 53.9%; Pred. No. 0.27;
Matches 69; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 38 CTAAGGATGTCAGAGATCCCAAGTCGACGAGAGAGATGGTGAGGCTATTATTCCCG 97
DB 400 CCAACAGATTGTCAGAGATGTCGGGCGAGGTCACAGAAAGTGGTGATCATTTAATTCACC 459
QY 98 CAGTGCCTTCCTGCTGGGCTATGGATGAACAGTGGCTGACTTCATCTAGGAAGAGCTA 157
DB 460 ATTGCTGGACAGGCAAGGCCAAGGATGTCCACAGGAAGTGATATCCAGCAAAACTCA 519
QY 158 TGGCTTCT 165
DB 520 GAGTTTAT 527
RESULT 11
ABL30202/c
ID ABL30202 standard; DNA; 3819 BP.
XX ABL30202;
AC ABL30202;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 42079.
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX Drosophila melanogaster.
XX WO200171042-A2.
PN 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX Claim 1; SEQ ID NO 42079; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 3819 BP; 1093 A; 806 C; 787 G; 1133 T; 0 other;

Query Match 17.9%; Score 32.8; DB 23; Length 3819;
Best Local Similarity 55.2%; Pred. No. 0.74;
Matches 64; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 38 CCTAAGGATGTCACAGATCAAGTGCAGAGGAGATGTGGTGGAGCTATTTATTCCTCC 97

Db 2420 CCAACAGATGTCGAGATGTCGGGAGGTCCAGAAAGTGGGTGATCAATTTATTCACC 2361

QY 98 CAGTGCCTCCCTGCTGGGTATGATGAACAGTGGCTGACTTCATCTAGGAAAGA 153

Db 2360 ATTTGCTGGACAGCAAGCAAGGATGTCACAGGAAGTGGATATCCAGCAAAA 2305

RESULT 12

AAK73760

D AAK73760 standard; DNA; 3698 BP.

XX

AC AAK73760;

XX

DT 07-NOV-2001 (first entry)

XX

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28572.

DE

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

XX

OS Homo sapiens.

XX

PN WO200157182-A2.

XX

PD 09-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US01354.

XX

PR 31-JAN-2000; 2000US-0179065.

PR

PR 04-FEB-2000; 2000US-0180628.

PR

PR 24-FEB-2000; 2000US-0184564.

PR

PR 02-MAR-2000; 2000US-0186350.

PR

PR 16-MAR-2000; 2000US-0189874.

PR

PR 17-MAR-2000; 2000US-0190076.

PR

PR 18-APR-2000; 2000US-0198123.

PR

PR 19-MAY-2000; 2000US-0205515.

PR

PR 07-JUN-2000; 2000US-0209467.

PR

PR 28-JUN-2000; 2000US-0214886.

PR

PR 30-JUN-2000; 2000US-0215135.

PR

PR 07-JUL-2000; 2000US-0216647.

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PR 07-JUL-2000; 2000US-0216880.

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PR 11-JUL-2000; 2000US-0217487.

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PR 11-JUL-2000; 2000US-0217496.

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PR 14-JUL-2000; 2000US-0218290.

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PR 26-JUL-2000; 2000US-0220963.

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PR 26-JUL-2000; 2000US-0220964.

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PR 14-AUG-2000; 2000US-0224518.

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PR 14-AUG-2000; 2000US-0224519.

PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
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PR 17-NOV-2000; 2000US-0249208.

OS Homo sapiens.
XX WO200157182-A2.
XX 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US01354.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
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PR 05-JAN-2001; 2001US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PR (HUMA-) HUMAN GENOME SCI INC.
XX PA

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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure; SEQ ID NO 24625; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins, and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For

CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I) by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 10548 BP; 3143 A; 2302 C; 2158 G; 2945 T; 0 other;
Query Match 17.0%; Score 31.2; DB 22; Length 10548;
Best Local Similarity 55.6%; Pred. No. 3.9;
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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QY 134 CTGACTTCATCTAGGAAGAGCTATGGCTTCCTGCTCTCTGGAGCTCAC 181
Db 7500 CAAGTTCTATTCTAAAGAACCTAAATGGCGCGTGTGTGGTGGCTCAC 7547
Search completed: May 25, 2003, 03:13:59
Job time : 250 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 03:09:12 ; Search time 1754 Seconds
(without alignments)
1689.723 Million cell updates/sec

Title: US-09-660-568-49

Perfect score: 183

Sequence: 1 cacacactccccattctga.....ctgtctctcggagctcaacca 183

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
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18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pin.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
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27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 3	37	20.2	506	17	AQ419671 RPCI-11-1
c 4	36.6	20.0	789	17	BH317352 CH230-119
c 5	35.4	19.3	702	12	BG719810 602691217
c 6	34.2	18.7	831	12	BF571585 602078004

7	34	18.6	283	12	BG161919
8	33.6	18.4	695	9	AI512580
c 9	33	18.0	438	9	AI243308
c 10	33	18.0	467	9	AI806410
c 11	33	18.0	481	17	BH274856
c 12	33	18.0	594	17	BH268816
c 13	32.8	17.9	582	13	BM663839
c 14	32.8	17.9	994	17	CNS01744
c 15	32.4	17.7	226	17	AQ543989
c 16	32.4	17.7	524	17	B01998
c 17	32.4	17.7	544	17	AQ809155
c 18	32.4	17.7	609	12	BG720090
c 19	32	17.5	365	17	AZ745700
c 20	32	17.5	401	17	BH305232
c 21	31.8	17.4	455	17	AQ536443
c 22	31.8	17.4	591	12	BG606222
c 23	31.6	17.3	638	17	AG034524
c 24	31.6	17.3	649	13	BM416296
c 25	31.6	17.3	720	17	BH307258
c 26	31.4	17.2	258	14	H32274
c 27	31.4	17.2	308	17	AQ252041
c 28	31.4	17.2	574	13	BI359567
c 29	31.4	17.2	623	10	BE082216
c 30	31.4	17.2	634	9	AL510875
c 31	31.4	17.2	695	17	BH364239
c 32	31.2	17.0	316	17	AQ584142
c 33	31.2	17.0	446	17	AQ977475
c 34	31.2	17.0	524	17	AQ177467
c 35	31.2	17.0	535	17	AQ284523
c 36	31.2	17.0	751	17	AZ633721
c 37	31	16.9	502	17	AZ217607
c 38	31	16.9	566	17	AZ792647
c 39	31	16.9	1082	17	CNS078V
c 40	30.8	16.8	417	12	BG190341
c 41	30.8	16.8	425	17	BH258367
c 42	30.8	16.8	481	17	BH860938
c 43	30.8	16.8	514	17	AQ792988
c 44	30.8	16.8	517	14	BQ090484
c 45	30.8	16.8	577	17	AQ189764

ALIGNMENTS

RESULT 1
BG775699/c
LOCUS 602650070T1 NIH_MGC_40 Homo sapiens CDNA clone IMAGE:4760993 3',
DEFINITION BG775699 961 bp mRNA linear EST 15-MAY-2001
ACCESSION BG775699
VERSION BG775699.1 GI:14046016.
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 961)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1612 row: 1 column: 18
High quality sequence start: 4
High quality sequence stop: 783.
Location/Qualifiers

FEATURES

Db 645 CTTTCTCTGTCGAAGACCTGCTGGTGAACCTGGGACACACAGAGGCAGAAATTCCTC 586

**LOCUS
DEFINITION**

```

mRNA sequence.
ACCESSION BF571585
VERSION BF571585.1 GI:11645297
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 831)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1077 row: h column: 02
High quality sequence stop: 571..
FEATURES
Location/Qualifiers
1..831
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4252465"
/clone_lib="NIH_MGC_62"
/tissue_type="melanotic melanoma, high MDR"
/lab_host="DH10B (T1 phage-resistant)"
/Note="Organ: skin; Vector: pDMR-LIB (Clontech); Site_1:
SfiI (ggccgctggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGCGGCGGAGATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT 219 a 190 c 216 g 206 t
ORIGIN
Query Match 18.7%; Score 34.2; DB 12; Length 831;
Best Local Similarity 58.3%; Pred. No. 7.9;
Matches 60; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

64 CAGAAGGAGATGTGTGAGGCTATTATTCCTCCAGTGCCTTCCTGGGCTATGCA 123
||||| ||| ||| ||||||| ||||| ||| ||| ||| ||| ||| ||| |||
Db 334 CAGATCGAGGACTGTGTGTGCTTATTCATCTCTCCATTGGCTAAACAGATGAACAAGCGA 393

QY 124 TGAACAGTGCACATTCATCTAGGAAGAGAGCTATGCTTCG 166
||||| ||| ||| ||||||| ||||| ||| ||| ||| ||| ||| ||| |||
Db 394 GGTGTCTACACTAACAGCAGCAGCTGGGAAGAGATTAGCTGTG 436

RESULT 7
BG161919
LOCUS BG161919 283 bp mRNA linear EST 06-FEB-2001
DEFINITION dc43b12.y1 NICHD XGC Emb3 Xenopus laevis cDNA clone IMAGE:3399886
5', mRNA sequence.
ACCESSION BG161919
VERSION BG161919.1 GI:12695838
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
REFERENCE 1 (bases 1 to 283)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other ESTs: dc43b12.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 269.
FEATURES
Location/Qualifiers
1..283
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone_lib="IMAGE:3399886"
/clone_lib="NICHD XGC Emb3"
/tissue_type="embryo (stages 24-25)"
/lab_host="DH10B (phage-resistant)"
/Note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 1.7 kb. Constructed by Life Technologies. Note: This
is a Xenopus Gene Collection (XGC) library."
BASE COUNT 76 a 58 c 68 g 81 t
ORIGIN
Query Match 18.6%; Score 34; DB 12; Length 283;
Best Local Similarity 61.1%; Pred. No. 5.1;
Matches 55; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 63 GCAGAGAGAGATGTGTGAGGCTATTATTCCTCCAGTGCCTTCCTGGGCTATGG 122
||||| ||| ||| ||||||| ||||| ||| ||| ||| ||| ||| ||| |||
Db 157 GCAGATGAAGATTGTGTAGGCTATTATTCACAGAGCAATGCTCTCTGGCTTCAT 216

QY 123 ATGACAGTGGCTGACTTCATCTAGGAAG 152
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 217 ATTGTAGAGGCTTGTAGACCAAGGAGG 246

RESULT 8
AI512580
LOCUS AI512580 695 bp mRNA linear EST 23-APR-2001
DEFINITION LD44491.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
melanogaster cDNA clone LD44491 5 similar to Cyp310a1: FBan0010391
'cytochrome P450' located on: 2L 37A3-37A3;: 04/10/2001, mRNA
sequence.
ACCESSION AI512580
VERSION AI512580.2 GI:13770009
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
REFERENCE 1 (bases 1 to 695)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
On Mar 16, 1999 this sequence version replaced gi:4421998.
Other ESTs: LD44491.3prime
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003659; arm:2L [18246373,18507269]
estimated-cyto:36F7-37A4; 04/10/2001
Plate: LD.444 row: H column: 7

```


QY 101 TGCCTTCCTGCTGGCTATGATGAACAGTGGCTGACTTCATCT 145
 DB 143 CACCTTCCTTCCTGCTATGGCTTGACAGTGGTTGTTTCT 99

RESULT 11

BH274856

LOCUS BH274856 481 bp DNA linear GSS 30-NOV-2001
 DEFINITION CH230-48J1.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone

CH230-48J1, DNA sequence.

ACCESSION BH274856

VERSION BH274856.1 GI:17187258

KEYWORDS GSS.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 481)
 AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P., and Fraser, C.M.

TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment
 JOURNAL Unpublished (1999)
 COMMENT Other_GSSs: CH230-48J1.TV

Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or ering_information.htm). BAC end
 page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html
 Plate: 48 row: J column: 1
 Seq primer: SP6
 Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..481
 /organism="Rattus norvegicus"
 /strain="BN/SSNHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-48J1"
 /clone_lib="CHORI-230 Segment 1"
 /sex="Female"
 /cell_type="Brain"

/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
 CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
 Pieter de Jong"

BASE COUNT 129 a 141 c 125 g 86 t

ORIGIN

Query Match 18.0%; Score 33; DB 17; Length 481;
 Best Local Similarity 60.7%; Pred. No. 14;
 Matches 54; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 88 TTTATTCCCCAGTCCCTCCCTGCTGGCTATGGATGACAGTGGCTGACTTCATCTAG 147

DB 265 TTTCTGCTCAAGAGACCTGCTGCTGGTGAACCTCAGGACACAGAGGAGGAGTCTCTAG 324

QY 148 GAAAGAGCTATGCTCTCTGCTCTCTGGAG 176

DB 325 GACCGGGACCTTCTGTGTTTACCAGGAG 353

RESULT 12

BH268816

LOCUS BH268816 594 bp DNA linear GSS 30-NOV-2001

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CH230-186E20.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
 CH230-186E20, DNA sequence.

BH268816

BH268816.1 GI:17181122

GSS.

Norway rat.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 594)

Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P., and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment
 Unpublished (1999)

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering_information.htm). BAC end
 page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html

Plate: 186 row: E column: 20

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..594

/organism="Rattus norvegicus"

/strain="BN/SSNHsd/MCW"

/db_xref="taxon:10116"

/clone="CH230-186E20"

/clone_lib="CHORI-230 Segment 1"

/sex="Female"

/cell_type="Brain"

/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;

CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by

Pieter de Jong"

BASE COUNT 158 a 187 c 155 g 94 t

ORIGIN

Query Match 18.0%; Score 33; DB 17; Length 594;
 Best Local Similarity 60.7%; Pred. No. 16;
 Matches 54; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 88 TTTATTCCCCAGTCCCTCCCTGCTGGCTATGGATGACAGTGGCTGACTTCATCTAG 147

DB 235 TTTCTGCTCAAGAGACCTGCTGCTGGTGAACCTCAGGACACAGAGGAGGAGTCTCTAG 294

QY 148 GAAAGAGCTATGCTCTCTGCTCTCTGGAG 176

DB 295 GACCGGGACCTTCTGTGTTTACCAGGAG 323

RESULT 13

BH663839/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 582)

BH663839 582 bp mRNA linear EST 27-FEB-2002

UI-E-CL1-afe-k-03-0-UI.s1 UI-E-CL1 Homo sapiens cDNA clone

UI-E-CL1-afe-k-03-0-UI 3', mRNA sequence.

BH663839

BH663839.1 GI:18969506

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Bernaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL discovery
MEDLINE Genome Res. 6 (9), 791-806 (1996)
COMMENT 97044477
 Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Dr. M. Bento Soares, University of Iowa
 Genetics (www.resgen.com).
 The following repetitive elements were found in this cDNA
 sequence: 11-93, >ALU (matched complement)
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES Location/Qualifiers
 source
 1..582
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-E-CL1-afe-k-03-0-UI"
 /clone_lib="UI-E-CL1"
 /tissue_type="human retina"
 /dev_stage="adult"
 /lab_host="Dhl0B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 UI-E-CL1 is a normalized cDNA library containing the
 following tissue(s): retina. The library was constructed
 according to Bernaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CCGCG. This library was
 created for the program, Gene Discovery in the Visual
 System, supported by National Eye Institute (NEI).
 TAG LIB=UI-E-CL1
 TAG TISSUE=human retina
 TAG_SEQ=CCGCG"
BASE COUNT 171 a 128 c 98 g 185 t
ORIGIN

Query Match 17.9%; Score 32.8; DB 13; Length 582;
 Best Local Similarity 54.0%; Pred. No. 18;
 Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
 Qy 8 TCCCCCATCTGAGCCCAAGAGCGTCATCCCTTAAGAGATGTCAGAGATCCCAAGTCAGA 67
 Db 149 TCCCTTCATATCAAGCGACAGCGTGGTTCATTAGTAAGCTTTGGCATACATGCTAATGGCA 90
 Qy 68 AGGAGATGTTGGTGGAGCTATTATTCGCCAGTGCCTTCCTCTGGCTATGGATGAA 127
 Db 89 GCGAGAGTTTGCAGTGTAGTGCAGATTCGCCACTGCACTCCAGCTGGGCGACTGACAA 30
 Qy 128 CAGT 131
 Db 29 GACT 26

RESULT 14
CNS0174A/c
LOCUS CNS0174A 994 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC

BACN17G20 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
ACCESSION AL107572
VERSION AL107572.1 GI:5627876
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 994)
 Genoscope.
 Direct Submission
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
 http://www.edgp.ebi.ac.uk -- This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billaud at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelOBAC11.

FEATURES Location/Qualifiers
 source
 1..994
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="BACN17G20"
 /clone_lib="DrosBAC"
 /plasmid="pBelOBAC11"
 /note="end : SP6"
BASE COUNT 223 a 214 c 242 g 250 t 65 others
ORIGIN
 Query Match 17.9%; Score 32.8; DB 17; Length 994;
 Best Local Similarity 55.2%; Pred. No. 24;
 Matches 64; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
 Qy 38 CCTAAGATGTCAGAGATCCCAAGTCAGAAAGAGGAATGTGTGAGGTATTTATTCGCC 97
 Db 427 CCACAGATGTCAGAGATGTCGGCAGGTCAGAAAGTGGTGATCATTTATTCACC 368
 Qy 98 CAGTGCCTTCCTGCTGGCTATGGATGAACAGTGGCTGACTTCATCTAGGAAGA 153
 Db 367 ATTGCTGGACAGGCAAGGCAAGGATGTCCACAGGAAGTGATATCCAGCAAAAA 312

RESULT 15
AQ543989/c
LOCUS AQ543989 226 bp DNA linear GSS 19-MAY-1999
DEFINITION RPCI-11-357B13.TV RPCI-11 Homo sapiens genomic clone RPCI-11-357B13
 , DNA sequence.
ACCESSION AQ543989
VERSION AQ543989.1 GI:4869383
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 226)
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
 ,J.C.
 Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 Unpublished (1997)
JOURNAL Other_GSSs: RPCI-11-357B13.TJ
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208

Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 03:09:47 ; Search time 52 Seconds
(without alignments)
1079.266 Million cell updates/sec

Title: US-09-660-568-49

Perfect score: 183

Sequence: 1 cacacactccccattctga.....ctgtctcttggaactcacca 183

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183	100.0	183	4	US-09-046-894-49
2	28.2	15.4	2846	4	Sequence 1, Appl
3	28	15.3	2297	4	Sequence 12, Appl
4	27.6	15.1	2367	3	Sequence 17, Appl
5	27.4	15.0	3243	2	Sequence 6, Appl
6	27.4	15.0	3243	2	Sequence 6, Appl
7	27.4	15.0	3243	3	Sequence 6, Appl
8	27	14.8	246240	2	Sequence 20, Appl
9	27	14.8	246240	2	Sequence 21, Appl
10	27	14.8	246240	2	Sequence 22, Appl
11	26.6	14.5	2624	1	Sequence 15, Appl
12	26.6	14.5	2624	3	Sequence 15, Appl
13	26	14.2	3138	4	Sequence 1, Appl
14	26	14.2	3834	3	Sequence 18, Appl
15	26	14.2	3854	1	Sequence 1, Appl
16	26	14.2	3858	2	Sequence 98, Appl
17	26	14.2	3858	4	Sequence 8, Appl
18	26	14.2	3863	4	Sequence 1, Appl
19	26	14.2	3863	6	Sequence 1, Appl
20	25.8	14.1	2380	6	Patent No. 5217870
21	25.6	14.0	1473	4	Patent No. 5268463
22	25.6	14.0	1473	4	Sequence 7, Appl
23	25.4	13.9	1001	4	Sequence 214, App
24	25.4	13.9	1001	4	Sequence 215, App
25	25.4	13.9	2777	4	Sequence 3, Appl
26	25.4	13.9	2777	4	Sequence 3, Appl
27	25.4	13.9	2790	3	Sequence 21, Appl

Sequence 1, Appl
Sequence 3, Appl
Sequence 2573, Ap
Sequence 2432, Ap
Sequence 250, App
Sequence 258, App
Sequence 4, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 26, Appl
Sequence 3, Appl

US-09-046-894-49
Sequence 49, Application US/09046894
Patent No. 6190857
GENERAL INFORMATION:
APPLICANT: Ralph, David
APPLICANT: An' Gang
APPLICANT: O'Hara, Mark S.
TITLE OF INVENTION: DIAGNOSIS OF DISEASE STATE USING mRNA
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,894
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,576
FILING DATE: 24-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:014
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-046-894-49

ALIGNMENTS

RESULT 1

US-09-046-894-49

Sequence 49, Application US/09046894

Patent No. 6190857

GENERAL INFORMATION:

APPLICANT: Ralph, David

APPLICANT: An' Gang

APPLICANT: O'Hara, Mark S.

TITLE OF INVENTION: DIAGNOSIS OF DISEASE STATE USING mRNA

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/046,894

FILING DATE: Concurrently Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/041,576

FILING DATE: 24-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Nakashima, Richard A.

REGISTRATION NUMBER: P-42,023

REFERENCE/DOCKET NUMBER: UROC:014

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 183 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-046-894-49

Query Match 100.0%; Score 183; DB 4; Length 183;

Best Local Similarity 100.0%; Pred. No. 8.6e-56;

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: MDI 251.4-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3243 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-239-276-6

Query Match 15.0%; Score 27.4; DB 2; Length 3243;
Best Local Similarity 57.6%; Pred. No. 5.4;
Matches 49; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 35 ATCCCTAAGGATGTCCAGAGATCCAAAGTCGAGAGGAGAAATGTGGTGGAGCTATTTATTC 94
   || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 161 ATGTCAAAGGACCAAGACAGAGCTACGACAGAAGGAGCTCCAGCTTCTGGTCATGATTC 220

QY 95 CCCAGTGCCTTCCTCCTCGGGCTA 119
   || || |||| |||| |||| ||||
Db 221 ACCAGCTGTCCACCTCGGGGACCA 245

RESULT 6
US-08-468-579B-6
; Sequence 6, Application US/08468579B
; Patent No. 5981700
; GENERAL INFORMATION:
; APPLICANT: Rabin, Daniel
; TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
; TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spring Kramer Schaefer & Briscoe
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.5
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,579B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,276
; FILING DATE: 05-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,646
; FILING DATE: 08-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/715,181
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/441,703
; FILING DATE: 04-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/312,543
; FILING DATE: 17-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: MDI 251.5-KGB
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3243 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-468-579B-6

Query Match 15.0%; Score 27.4; DB 2; Length 3243;
Best Local Similarity 57.6%; Pred. No. 5.4;
Matches 49; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 35 ATCCCTAAGGATGTCAGAGATCCCAAGTGCAGAGGAGAATGTGCTGAGGCTATTATTC 94
DB 161 ATGTCAAAGGGACCAAGAGAGCCCTAGCAGAGAGAGAGCTCCAGCTTCTGTCATGATTC 220
QY 95 CCCAGTGCCTTCCCTGCTGGGCTA 119
DB 221 ACCAGCTGTCCACCTCGGGACCA 245

RESULT 7
US-08-468-577B-6
Sequence 6, Application US/08468577B
Patent No. 6001804

GENERAL INFORMATION:
APPLICANT: Rabid, Daniel
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Sprung Kramer Schaefer & Briscoe
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-5144

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.5
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,577B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,276
FILING DATE: 05-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
FILING DATE: 08-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/441,703
FILING DATE: 04-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/312,543
FILING DATE: 17-FEB-1989

ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 251.8-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3243 nucleotides

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-468-577B-6

Query Match 15.0%; Score 27.4; DB 3; Length 3243;
Best Local Similarity 57.6%; Pred. No. 5.4;
Matches 49; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 35 ATCCCTAAGGATGTCAGAGATCCCAAGTGCAGAGGAGAATGTGCTGAGGCTATTATTC 94
DB 161 ATGTCAAAGGGACCAAGAGAGCCCTAGCAGAGAGAGAGCTCCAGCTTCTGTCATGATTC 220
QY 95 CCCAGTGCCTTCCCTGCTGGGCTA 119
DB 221 ACCAGCTGTCCACCTCGGGACCA 245

RESULT 8
US-08-724-394A-20/c
Sequence 20, Application US/08724394A
Patent No. 5872237

GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-20
Query Match 14.8%; Score 27; DB 2; Length 246240;
Best Local Similarity 62.7%; Pred. No. 54;
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

TITLE OF INVENTION: N-Acetylglucosaminyltransferase V
TITLE OF INVENTION: Protein and Gene
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: USA
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/905,795
FILING DATE: 29-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/905,795
FILING DATE: 29-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 34-92A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
TELEFAX: (303)499-8089
TELEX: 823189
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2624 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 299..2521
US-08-016-863-15

Query Match 14.5%; Score 26.6; DB 1; Length 2624;
Best Local Similarity 48.4%; Pred. No. 9.5;
Matches 74; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
9 CCCCCATTCTGAGCCCAAGAGGCTCATCCCTAAGGATGTCCAGAGATCCCAAGTGCAGAA 68
Db 2489 CCTTGATGAAGTCCCGGCGAGGAGATCCGCTGGTGTGGGGTGGGGCCGCGACAC 2430
99 GGAGATGTGGTGGAGGCTATTTATCCCGAGTGCCTTCCCTGCTGGGCTATGGATGAAC 128
Db 2429 TGAAGACGAGGATCCCTTGGACACACAGTGTCTTCTTGGGTAGAGAGGGGCA 2370
99 AGTGGCTGACTTCATCTAGAAAGAGCTATGCC 161
Db 2369 CCAGGATGCTCTGTATAGTTCTGAGCTTTGCC 2337

RESULT 12
US-08-276-968A-15/c
Sequence 15, Application US/08276968A
Patent No. 6015701
GENERAL INFORMATION:
APPLICANT: pierce, James M.
APPLICANT: Shoreliah, Mohamed G.
APPLICANT: Adler, Beverly L.
APPLICANT: Fregien, Nevils L.
TITLE OF INVENTION: N-Acetylglucosaminyltransferase V
TITLE OF INVENTION: Proteins and Sequences
NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: USA
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,968A
FILING DATE: 19-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/905,795
FILING DATE: 29-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/016,863
FILING DATE: 10-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 34-92D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)-499-8080
TELEFAX: (303)-499-8089
TELEX: 49617824
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2624 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 299..2521
US-08-276-968A-15

Query Match 14.5%; Score 26.6; DB 3; Length 2624;
Best Local Similarity 48.4%; Pred. No. 9.5;
Matches 74; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
9 CCCCCATTCTGAGCCCAAGAGGCTCATCCCTAAGGATGTCCAGAGATCCCAAGTGCAGAA 68
Db 2489 CCTTGATGAAGTCCCGGCGAGGAGATCCGCTGGTGTGGGGTGGGGCCGCGACAC 2430
99 GGAGATGTGGTGGAGGCTATTTATCCCGAGTGCCTTCCCTGCTGGGCTATGGATGAAC 128
Db 2429 TGAAGACGAGGATCCCTTGGACACACAGTGTCTTCTTGGGTAGAGAGGGGCA 2370
99 ACTGGCTGACTTCATCTAGAAAGAGCTATGCC 161
Db 2369 CCAGGATGCTCTGTATAGTTCTGAGCTTTGCC 2337

RESULT 13
US-09-434-408-1
Sequence 1, Application US/09434408
Patent No. 6440697
GENERAL INFORMATION:
APPLICANT: Venezia, Domenick
APPLICANT: Grossmann, Angelika
TITLE OF INVENTION: RING FINGER PROTEIN ZAFOP3
FILE REFERENCE: 98-41
CURRENT APPLICATION NUMBER: US/09/434,408
CURRENT FILING DATE: 1999-11-04
EARLIER APPLICATION NUMBER: US 60/108,258

EARLIER FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 3138
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (367)...(2535)
US-09-434-408-1

Query Match 14.2%; Score 26; DB 4; Length 3138;
Best Local Similarity 52.8%; Pred. No. 17;
Matches 56; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 8 TCCCCATTGTGAGCCCAAGAGCTCATCCCTAAGGATGTCCAGAGATCCAAAGTGCAGA 67
DB 473 TCCTAATGTGAGCTTCAGAGATCCATTTGGAGCTTTGCAACATGCAAGTTCTGC 532

68 AGGAGATGTGTGAGCTATTTATTTCCCAAGTGCCTTCCCTGCT 113
DB 533 AGAAGAGTGTGCTGATCGTCCACAGAAATCACTCACTTCCCTGCT 578

RESULT 14

US-09-209-668-18
Sequence 18, Application US/09209668A
Patent No. 6114517

GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Xu, Xiaoxing S.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
FILE REFERENCE: ISPH-0336
CURRENT APPLICATION NUMBER: US/09/209,668A
CURRENT FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 18
LENGTH: 3834
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (117)...(1949)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: M24736/Genbank
DATABASE ENTRY DATE: 1994-11-07
US-09-209-668-18

Query Match 14.2%; Score 26; DB 3; Length 3834;
Best Local Similarity 49.3%; Pred. No. 18;
Matches 68; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 21 GCCCAAGAGGCTATCCCTAAGGATGTCCAGAGATCCAAAGTGCAGAAGAGATGTGGT 80
DB 2072 GCTGAACCCGCAACACCCATCCACCTTCAATAGATCAAAAGTCCAGCAGGACGCGC 2131
QY 81 GAGGCTATTTATTTCCCAAGTGCCTTCCCTGCTGGGCTATGGATGACAGTGGCTGACTT 140
DB 2132 CTTCACCTGAAAGAGACTCAGTGTTCCTTCTTCTACTCTCAGGATCAAGAAAGTGTGGCT 2191
QY 141 CATCTAGAAAGAGCTAT 158
DB 2192 AATGAAGGGAAGGATAT 2209

RESULT 15

US-08-365-470-1
Sequence 1, Application US/08365470
Patent No. 5632991
GENERAL INFORMATION:

APPLICANT: Gimbrone, Jr., Michael A.
TITLE OF INVENTION: Antibodies Specific For E-selectin And The Uses
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,470
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,510
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA: US 07/850,802
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 0627.1350003
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3854 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-365-470-1

Query Match 14.2%; Score 26; DB 1; Length 3854;
Best Local Similarity 49.3%; Pred. No. 18;
Matches 68; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 21 GCCCAAGAGGCTATCCCTAAGGATGTCCAGAGATCCAAAGTGCAGAAGAGATGTGGT 80
DB 2072 GCTGAACCCGCAACACCCATCCACCTTCAATAGATCAAAAGTCCAGCAGGACGCGC 2131
QY 81 GAGGCTATTTATTTCCCAAGTGCCTTCCCTGCTGGGCTATGGATGACAGTGGCTGACTT 140
DB 2132 CTTCACCTGAAAGAGACTCAGTGTTCCTTCTTCTACTCTCAGGATCAAGAAAGTGTGGCT 2191
QY 141 CATCTAGAAAGAGCTAT 158
DB 2192 AATGAAGGGAAGGATAT 2209

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

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Title: US-09-660-568-49

Perfect score: 183

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Searched: 828747 seqs, 560231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	30.6	16.7	5216	9	US-10-074-095-695
4	30.6	16.7	5216	10	US-09-764-870-607
5	30.6	16.7	5216	10	US-09-764-860-695
6	28.8	15.7	8894	9	US-10-092-154-1606
7	28.8	15.7	8894	10	US-09-764-847-1606
8	28.4	15.5	2001	9	US-09-829-155C-8
9	28.4	15.5	2513	9	US-09-829-155C-10
10	28.2	15.4	358	9	US-10-060-036-1937
11	28.2	15.4	1243	12	US-10-044-090-96
12	28.2	15.4	1907	9	US-10-023-282-108
13	28.2	15.4	2084	9	US-10-023-282-234
14	28.2	15.4	2329	12	US-10-044-090-416
15	27.8	15.2	374	9	US-09-918-995-6295
16	27.8	15.2	20907	9	US-09-764-891-9966
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18	27.6	15.1	312	10	US-09-783-590-11431
19	27.6	15.1	945	9	US-10-023-601-43

ALIGNMENTS

RESULT 1

US-09-864-761-21666
; Sequence 21666, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

20 27.6 15.1 1295 10 US-09-881-852-17 Sequence 17, Appl
21 27.6 15.1 26668 10 US-09-962-832-222 Sequence 222, App
22 27.6 15.1 39776 9 US-10-160-293-3 Sequence 3, Appl1
C 23 27.4 15.0 534 10 US-09-920-300A-1518 Sequence 1518, Ap
C 24 27.4 15.0 534 12 US-10-033-528-1518 Sequence 1518, Ap
C 25 27.4 15.0 904 9 US-10-082-830-120 Sequence 120, App
C 26 27.4 15.0 1309 9 US-10-082-830-121 Sequence 121, App
C 27 27.2 14.9 8048 9 US-09-764-872-917 Sequence 1495, Ap
C 28 27.2 14.9 16825 9 US-09-764-847-1495 Sequence 1495, Ap
C 29 27.2 14.9 16825 10 US-09-294-093B-1409 Sequence 1409, Ap
C 30 27 14.8 294 10 US-09-918-995-37556 Sequence 37556, A
C 31 27 14.8 371 9 US-09-920-300A-583 Sequence 583, App
32 27 14.8 422 12 US-10-033-528-583 Sequence 482, App
33 27 14.8 501 10 US-09-918-995-32131 Sequence 32131, A
C 35 27 14.8 502 9 US-09-918-995-32131 Sequence 32131, A
C 36 27 14.8 511 9 US-09-918-995-32131 Sequence 32131, A
37 27 14.8 56686 10 US-09-736-960-86 Sequence 86, Appl
38 26.8 14.6 1497 9 US-10-011-582-3 Sequence 3, Appl1
39 26.8 14.6 2175 9 US-10-011-582-3 Sequence 3, Appl1
40 26.8 14.6 2223 9 US-09-891-762-3 Sequence 9, Appl1
41 26.8 14.6 2286 9 US-10-011-582-5 Sequence 5, Appl1
42 26.8 14.6 2373 9 US-10-011-582-5 Sequence 8, Appl1
43 26.8 14.6 2612 9 US-09-891-762-1 Sequence 1, Appl1
44 26.8 14.6 4586 9 US-09-764-891-5830 Sequence 5830, Ap
45 26.8 14.6 5746 9 US-09-764-891-5830 Sequence 5830, Ap

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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21666
; LENGTH: 164
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF000498.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: NT HIT: AB026898.1, EVALUE 9.00e-88
; OTHER INFORMATION: SWISSPROT HIT: P79023, EVALUE 1.70e-00
; OTHER INFORMATION: EST_HUMAN HIT: BF346467.1, EVALUE 1.40e-01
US-09-864-761-21666

Query Match          19.2%; Score 35.2; DB 10; Length 164;
Best Local Similarity 71.9%; Pred. No. 0.006; 18; Indels 0; Gaps 0;
Matches 46; Conservative 0; Mismatches 0;

QY 52 GAGATCAAGTCAGAGGAGAGATGCTGAGGCTATTATTCCTCCAGTGCTTCCCTG 111
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 100 GAGATCAGAGCAGAGAGAGAGATGAGTGAATATTATTCCTTGCTCTCTCTG 159
QY 112 CTGG 115
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DB 160 TGGG 163

RESULT 2
US-10-125-540-607/C
; Sequence 607, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 607
; LENGTH: 5216
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-540-607

Query Match          16.7%; Score 30.6; DB 9; Length 5216;
Best Local Similarity 56.4%; Pred. No. 0.92;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 23 CCCAAGAGGCTATCCCTTAAGATGTCCAGAGATCCAGATCCAGAGAGGAGATGTGTA 82
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DB 2539 CTCGGAGGCTAAGGCAGGAGAGATGTGTGAACCCGGAAGGCAGAGCACTTGCAC 2480
QY 83 GGCATTATTTCCCTCCAGTGCCTTCCCTGCTGGCTATGA 123
| || || || || || || || || || || || || || || || || || || || || ||
DB 2479 GAGCTTAGATTGGCCACACTGCACATCCAGGCTGGGCAACAGA 2439
| || || || || || || || || || || || || || || || || || || || || ||
; PRIOR APPLICATION NUMBER: US/10/074,095
; Sequence 695, Application US/10074095
; Publication No. US20030077704A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008C1
; CURRENT APPLICATION NUMBER: US/10/074,095
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 09/764,860
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
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; PRIOR FILING DATE: 2000-08-14
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; PRIOR FILING DATE: 2000-09-29
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; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
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; PRIOR FILING DATE: 2000-09-29
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; PRIOR APPLICATION NUMBER: 60/229,343
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; PRIOR FILING DATE: 2000-09-01
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; PRIOR APPLICATION NUMBER: 60/229,513
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; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
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; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
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; PRIOR FILING DATE: 2000-11-08
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; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
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; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
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; PRIOR APPLICATION NUMBER: 60/249,213
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; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,214
; PRIOR FILING DATE: 2000-11-17
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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08

Query Match 16.7% Score 30.6; DB 9; Length 5216;
Best Local Similarity 56.4% Pred. No. 0.92;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 23 CCCAAGAGGCTCATCCCTTAAGATGTCAGAGATCCAAAGTCCAGAGAGGAATGTGTGA 82
DB 2678 CTCGGAGGCTAAGCAGGAGATGGTGTGAACCCGGAAGCAGAGGCAACTTGCAGT 2737
QY 83 GGCATTATTATTCCTCCAGTGCCTCCCTGCTGGGCTATGGA 123
DB 2738 GAGCTTAGATTGCGCCACTGCACCTCCAGGCTGGGCAACAGA 2778

RESULT 4
US-09-764-870-607/c
; Sequence 607, Application US/09764870

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; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 607
; LENGTH: 5216
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-870-607

Query Match      16.7%; Score 30.6; DB 10; Length 5216;
Best Local Similarity 56.4%; Pred. No. 0.92;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

23 CCCAAGAGGCTCATCCTTAAGGATGCCAGATCCAAAGTGCAGAGGAGAAATGTGGTGA 82
Db 2539 CTCGGGAGGCTAAGGCAGGAGAAATGTGTGAACCCGGAAGGCAGAGGCAACTTGCAC 2480
QY 83 GCGTATTATTTCCCTCCAGTGCCTTCCCTGCTGGCTATGGA 123
Db 2479 GAGCTTAGATTGGCACTGCACCTCCAGGCTGGCAACAGA 2439

RESULT 5
US-09-764-860-695
; Sequence 695, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 695
; LENGTH: 5216
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-695

Query Match      16.7%; Score 30.6; DB 10; Length 5216;
Best Local Similarity 56.4%; Pred. No. 0.92;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 23 CCCAAGAGGCTCATCCTTAAGGATGCCAGATCCAAAGTGCAGAGGAGAAATGTGGTGA 82
Db 2678 CTCGGGAGGCTAAGGCAGGAGAAATGTGTGAACCCGGAAGGCAGAGGCAACTTGCAC 2737
QY 83 GCGTATTATTTCCCTCCAGTGCCTTCCCTGCTGGCTATGGA 123
Db 2738 GAGCTTAGATTGGCACTGCACCTCCAGGCTGGCAACAGA 2778

RESULT 6
US-10-092-154-1606
; Sequence 1606, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm

; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 607
; LENGTH: 5216
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-870-607

Query Match      15.7%; Score 28.8; DB 9; Length 8894;
Best Local Similarity 58.0%; Pred. No. 5;
Matches 51; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 56 GAAGGAGAAATGTGGTGAAGCTATTATTTCCCTCCAGTGCCTTCCCTGCTGGGCTATGGATG 125
Db 3269 GAGGCAGAGGTTGCAGTGAAGATCGCACCTAGCTAGCCTAGCCTGGGTGACAGAGC 3328
QY 126 AACAGTGGCTGACTTCATCTAGGAAAGA 153
Db 3329 GACAGCAGCAGACTTCATCTAAGAAGA 3356

RESULT 7
US-09-764-847-1606
; Sequence 1606, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1606
; LENGTH: 8894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1606

Query Match      15.7%; Score 28.8; DB 10; Length 8894;
Best Local Similarity 58.0%; Pred. No. 5;
Matches 51; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 56 GAAGGAGAAATGTGGTGAAGCTATTATTTCCCTCCAGTGCCTTCCCTGCTGGGCTATGGATG 125
Db 3269 GAGGCAGAGGTTGCAGTGAAGATCGCACCTAGCTAGCCTAGCCTGGGTGACAGAGC 3328
QY 126 AACAGTGGCTGACTTCATCTAGGAAAGA 153
Db 3329 GACAGCAGCAGACTTCATCTAAGAAGA 3356

RESULT 8
US-09-829-155C-8/c
; Sequence 8, Application US/09829155C
; Patent No. US20020155561A1
; GENERAL INFORMATION:
; APPLICANT: Thayer, Edward C.
; TITLE OF INVENTION: Mammalian Disulfide Core Protein-4
; FILE REFERENCE: 00-29
; CURRENT APPLICATION NUMBER: US/09/829,155C
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/196,230
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-829-155C-8

Query Match      15.5%; Score 28.4; DB 9; Length 2001;
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EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
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EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SEQ ID NO 108
SOFTWARE: Patent In Ver. 2.0
LENGTH: 1907
TYPE: DNA
ORGANISM: Homo sapiens
US-10-023-282-108

Query Match 15.4%; Score 28.2; DB 9; Length 1907;
Best Local Similarity 61.6%; Pred. No. 4.8;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 53 AGATCCAGTGCAGAGGAGATGTGGTGGCTATTATTTCCCCAGTGCCTTCCCTGC 112
Db 1595 AGAATGGAGAGGAGGAGGCTGAGTTTGGGTATTGAATCCCGGCTCCACCTGC 1654
Qy 113 TGGGCTATGGATG 125
Db 1655 AGCATCAAGGTTG 1667

RESULT 13

US-10-023-282-234
Sequence 234, Application US/10023282
Publication No. US20030092893A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/10/023,282
CURRENT FILING DATE: 2001-12-20
EARLIER APPLICATION NUMBER: 09/205,258
EARLIER FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
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EARLIER APPLICATION NUMBER: 60/048,896
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EARLIER APPLICATION NUMBER: 60/048,876
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EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
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EARLIER APPLICATION NUMBER: 60/048,964
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EARLIER APPLICATION NUMBER: 60/048,882
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 234
LENGTH: 2084
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (775)
OTHER INFORMATION: n equals a.t.g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (2080)
OTHER INFORMATION: n equals a.t.g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (2083)
OTHER INFORMATION: n equals a.t.g, or c
US-10-023-282-234

Query Match 15.4%; Score 28.2; DB 9; Length 2084;
Best Local Similarity 51.6%; Pred. No. 5;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 53 AGATCCAAAGTGCAGAGGAGGAGTGTGGTGGCTATTTATTTCCCGAGTGCCTTCCCTGC 112
DB 1780 AGATGAGGAGGAGGAGGAGGCTGAGTTGGGTATTGAATCCCGGCTCCACCCCTGC 1839
QY 113 TGGGCTATGGATG 125
DB 1840 AGCATCAAGGTTG 1852

RESULT 14
US-10-044-090-416
Sequence 416, Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850

SOFTWARE: PERL Program
SEQ ID NO 416
LENGTH: 2329
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 2398075CB1
US-10-044-090-416

Query Match 15.4%; Score 28.2; DB 12; Length 2329;
Best Local Similarity 51.6%; Pred. No. 5.2; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 53 AGATCCAAAGTGCAGAGGAGGAGTGTGGTGGCTATTTATTTCCCGAGTGCCTTCCCTGC 112
DB 2048 AGATGAGGAGGAGGAGGAGGCTGAGTTGGGTATTGAATCCCGGCTCCACCCCTGC 2107
QY 113 TGGGCTATGGATG 125
DB 2108 AGCATCAAGGTTG 2120

RESULT 15
US-09-918-995-6295
Sequence 6295, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6295
LENGTH: 374
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-995-6295

Query Match 15.2%; Score 27.8; DB 9; Length 374;
Best Local Similarity 51.2%; Pred. No. 3.9;
Matches 65; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 52 GAGATCCAAAGTGCAGAGGAGGAGTGTGGTGGCTATTTATTTCCCGAGTGCCTTCCCTGC 111
DB 99 GAGCCAGCGCCGCGGATGTCAGCAGCAGGTTGGTCTACACACACACACCGCTCCCTGC 158
QY 112 CTGGGCTATGGATGAACAGTGGCTGACCTTCATCTAGGAAAGAGCTATGCTTCTCTCTCC 171
DB 159 CGTCTCGCGGCTGAGCTCTCTCTCGGCCCTCCACACAGGAGTTGAGTGGTCTCC 218
QY 172 TGGAGCT 178
DB 219 AGGAGCT 225

Search completed: May 25, 2003, 04:19:26
Job time : 142 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 03:08:42 ; Search time 1933 Seconds
(without alignments)
2755.206 Million cell updates/sec

Title: US-09-660-568-49

Perfect score: 183

Sequence: 1 cacacactccccattctga.....ctgtctcttgaggctcacca 183

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_man:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	183	100.0	183	6	ARI30466	ARI30466 Sequence
C 2	152.2	83.2	146327	9	ALI162253	ALI162253 Human DNA
C 3	44.4	24.3	189509	9	AC099564	AC099564 Homo sapi
C 4	43.6	23.8	91639	9	ALI162399	ALI162399 Human DNA
C 5	43.4	23.7	167115	9	AC090093	AC090093 Homo sapi
C 6	43.4	23.7	173087	2	AC107318	AC107318 Sus scrofa
C 7	43.4	23.7	184787	2	AC087354	AC087354 Homo sapi
C 8	43.4	23.7	185420	2	AC021973	AC021973 Homo sapi
C 9	42.4	23.2	205816	9	AC013751	AC013751 Homo sapi
C 10	41.8	22.8	174380	2	AC016075	AC016075 Homo sapi
C 11	41.8	22.8	175559	9	AC112498	AC112498 Homo sapi
C 12	41.8	22.8	177220	9	HS179D22	HS179D22 Homo sapi
C 13	41.6	22.7	58693	2	AC107875	AC107875 Homo sapi
C 14	41.6	22.7	111461	9	AP005368	AP005368 Homo sapi
C 15	41.6	22.7	149126	9	AC105177	AC105177 Homo sapi
C 16	41.6	22.7	162987	2	AP005359	AP005359 Homo sapi
C 17	41.2	22.5	162126	9	AL354711	AL354711 Human DNA
C 18	41	22.4	60059	9	AL354657	AL354657 Human DNA
C 19	41	22.4	150409	9	AP003496	AP003496 Homo sapi
C 20	41	22.4	152142	9	AP003494	AP003494 Homo sapi
C 21	41	22.4	191895	9	AC009481	AC009481 Homo sapi
C 22	40.8	22.3	134339	9	AC114501	AC114501 Homo sapi
C 23	40.8	22.3	158513	2	AC011054	AC011054 Homo sapi
C 24	40.8	22.3	163395	2	AC103726	AC103726 Homo sapi
C 25	40.6	22.2	57000	9	AC078862	AC078862 Homo sapi
C 26	40.2	22.0	132470	9	HS203P18	HS203P18 Human DNA
C 27	40	21.9	150533	9	AL356215	AL356215 Human DNA
C 28	40	21.9	154067	2	AC087656	AC087656 Homo sapi
C 29	40	21.9	162851	2	AC009637	AC009637 Homo sapi
C 30	40	21.9	176425	2	AC090418	AC090418 Homo sapi
C 31	39.8	21.7	155147	9	HS992D9	HS992D9 Human DNA
C 32	39.8	21.7	162249	2	AC020682	AC020682 Homo sapi
C 33	39.8	21.7	166973	9	AL451049	AL451049 Human DNA
C 34	39.6	21.6	107637	2	AC094679	AC094679 Rattus no
C 35	39.6	21.6	147301	2	AP001928	AP001928 Homo sapi
C 36	39.6	21.6	167376	9	AP001994	AP001994 Homo sapi
C 37	39.6	21.6	180402	2	AC016849	AC016849 Homo sapi
C 38	39.6	21.6	221091	9	AP003390	AP003390 Homo sapi
C 39	39	21.3	64491	9	AL365188	AL365188 Human DNA
C 40	39	21.3	172900	9	AC107027	AC107027 Homo sapi
C 41	38.4	21.0	51626	2	AC068840	AC068840 Homo sapi
C 42	38.4	21.0	103120	2	AC103223	AC103223 Rattus no
C 43	38.4	21.0	112622	2	AC010866	AC010866 Homo sapi
C 44	38.4	21.0	114800	9	AC123567	AC123567 Homo sapi
C 45	38.4	21.0	119234	2	AC105231	AC105231 Homo sapi

ALIGNMENTS

RESULT 1
ARI30466 ARI30466 Sequence 49 from patent US 6190857. 183 bp DNA Linear PAT 16-MAY-2001
LOCUS ARI30466
DEFINITION ARI30466
ACCESSION ARI30466
VERSION ARI30466.1 GI:14118791
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 183)
AUTHOR Ralph, D., An, G., O'Hara, S., Mark, and Veltri, R.
TITLE Diagnosis of disease state using mRNA profiles in peripheral leukocytes
JOURNAL Patent: US 6190857-A 49 20-FEB-2001;

FEATURES source Location/Qualifiers
1. .183
/organism="unknown"
BASE COUNT 43 a 52 c 45 g 43 t
ORIGIN

Query Match 100.0%; Score 183; DB 6; Length 183;
Best Local Similarity 100.0%; Pred. No. 3e-49;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACACATCCCCCATCTGAGCCCAAGAGGCTCATCCCTAGGATGTCAGAGATCCAA 60
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DB 1 CACACATCCCCCATCTGAGCCCAAGAGGCTCATCCCTAGGATGTCAGAGATCCAA 60
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QY 61 GTGCAAGAGGAATGTGTGAGGCTATTATTATCCCCAGTGCCTTCCTGCTGGGCTAT 120
|||||
DB 61 GTGCAAGAGGAATGTGTGAGGCTATTATTATCCCCAGTGCCTTCCTGCTGGGCTAT 120
|||||

QY 121 GGATGAACAGTGGCTGACATTCATCTAGGAAGAGCTATGGCTTCCTCTCGGAGCTCA 180
|||||
DB 121 GGATGAACAGTGGCTGACATTCATCTAGGAAGAGCTATGGCTTCCTCTCGGAGCTCA 180
|||||

QY 181 CCA 183
DB 181 CCA 183

RESULT 2
AL162253/c
LOCUS Human DNA sequence from clone RP11-574F11 on chromosome 9, complete
DEFINITION sequence.
ACCESSION AL162253
VERSION AL162253.17 GI:13677203
KEYWORDS HTG.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Clark, G.
Direct Submission
Submitted (20-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Apr 19, 2001 this sequence version replaced gi:12539553.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RP11-574F11 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6
IMPORTANT: This sequence is not the entire insert of clone

RP11-574F11 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP11-574F11 is at 146327 in this
sequence. The true left end of clone RP11-635N21 is at 62948 in
this sequence. The true right end of clone RP11-12D24 is at 100 in
this sequence.

FEATURES source Location/Qualifiers
1. .146327
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-574F11"
/clone_11b="RPCI-11.2"
84304. .84605
/note="Sequence from overlapping clone BA635N21
(AL354744). Assembly confirmed by restriction digest
data."
misc_feature 84304. .84306
/note="Single clone region. Assembly confirmed by
restriction digest data."
BASE COUNT 44360 a 29767 c 29483 g 42717 t
ORIGIN

Query Match 83.2%; Score 152.2; DB 9; Length 146327;
Best Local Similarity 92.5%; Pred. No. 4.1e-39;
Matches 160; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 ACACACTCCCCCATCTGAGCCCAAGAGGCTCATCCCTAAGATGTCAGAGATCCAAAG 61
|||||
DB 145681 ACTCTCCACTCTGCTTTCAGCCCAAGAGGCTCATCCCTAAGATGTCAGAGATCCAAAG 145622
|||||

QY 62 TGCAGAAGAGAAATGTGTGAGGCTATTATTTCCCCAGTGCCTTCCTGCTGGGCTATG 121
|||||
DB 145621 TGCAGAAGAGAAATGTGTGAGGCTATTATTTCCCCAGTGCCTTCCTGCTGGGCTATG 145562
|||||

QY 122 GATGAACAGTGGCTGACATTCATCTAGGAAGAGCTATGGCTTCCTCTCCCTGG 174
|||||
DB 145561 GATGAACAGTGGCTGACATTCATCTAGGAAGAGCTATGGCTTCCTCTCCCTGGTAG 145509
|||||

RESULT 3
AC099564/c
LOCUS Homo sapiens chromosome 1 clone RP11-359A17, complete sequence.
DEFINITION AC099564 AL391540
ACCESSION AC099564.2 GI:20163088
VERSION HTG.
KEYWORDS Homo sapiens
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.
Direct Submission
Unpublished
2 (bases 1 to 189509)
REFERENCE Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
AUTHORS Direct Submission
TITLE Submitted (16-NOV-2001) Genome Center, University of Washington,
JOURNAL Box 352145, Seattle, WA 98195, USA
AUTHORS 3 (bases 1 to 189509)
REFERENCE Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.
AUTHORS Direct Submission
TITLE Submitted (17-APR-2002) Genome Center, University of Washington,
JOURNAL Box 352145, Seattle, WA 98195, USA
COMMENT On Apr 17, 2002 this sequence version replaced gi:16946001.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1>

RP11-545110 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-545110 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RP11-545110 is at 1 in this sequence.

The true left end of clone RP4-681G13 is at 89640 in this sequence.

The true right end of clone RP11-576122 is at 40989 in this sequence.

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FEATURES
  source          Location/Qualifiers
    1..91639
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /chromosome="1"
      /clone="RP11-545I10"
      /clone_lib="RPC1-11.2"
      misc_feature 502..905
      /note="Sequence from overlapping clone RP11-576132
      (AL354732). Assembly confirmed by restriction digest."
BASE COUNT      29501 a 16967 g 17634 g 27537 t
ORIGIN
Query Match      23.8%; Score 43.6; DB 9; Length 91639;
Best Local Similarity 67.8%; Pred. No. 0.0025;
Matches 61; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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RESULT 5	
AC090093/c	
LOCUS	167115 bp DNA linear PRI 01-JUN-2002
DEFINITION	Homo sapiens chromosome 8, clone RP11-656A10, complete sequence.
AC090093	
AC090093.7	GI:21281556
HTG.	
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 167115)
AUTHORS	Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE	Homo sapiens chromosome 8, clone RP11-656A10
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 167115)
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,

	Query Match	Best Local Similarity	Score 24.3%;	Score 44.4;	DB 9;	Length 189509;
	Matches 63;	Conservative 0;	Mismatches 31;	Indels 0;	Gaps 0;	
QY	53	AGATCCAAAGTCGACGAGGAGAAATGTGGTCAGGCTATTTATTCGCCAGTGCCTTCCTCG	112			
DB	66065	AAATAAGATGGTGGCAAGAGAGGAGGATGAGATGATATTTCCCAAGGCTCCTTCCTCG	66006			
QY	113	TGGGCTATGGATGAACAGTGGCTGACTTCATCTA	146			
DB	66005	TAGGCTCTGGGTGGCAGTGGCTAACTTCCTCTA	65972			

RESULT 4	
AL162399	DNA linear PRI 25-OCT-2001
LOCUS	Human DNA sequence from clone RP11-545I10 on chromosome 1, complete
DEFINITION	sequence.
ACCESSION	AL162399
VERSION	AL162399.12 GI:16501106
KEYWORDS	HTG.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 91639)

TITLE	COMMENT
<p>Direct Submission</p> <p>Submitted (25-Oct-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk</p> <p>On Oct 26, 2001 this sequence version replaced gi:15130717.</p> <p>During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.</p> <p>This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at</p>	

Birren, B., Linton, L., Nusbaum, C., Landier, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collumore, A., Cook, A., Cooke, P., DeAtrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginder, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagoes, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczyk, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Marcuis, N.

request version

request version

Insert size: 185000; agarose-fp
 Insert size: 184820; sum-of-contigs
 Quality coverage: 6.44 in Q20 bases; agarose-fp
 Quality coverage: 5.98 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 7 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 2842: contig of 2842 bp in length
 * 2843 2942: gap of unknown length
 * 2943 6917: contig of 3975 bp in length
 * 6918 7017: gap of unknown length
 * 7018 15680: contig of 8663 bp in length
 * 15681 15780: gap of unknown length
 * 15781 30574: contig of 14794 bp in length
 * 30575 30674: gap of unknown length
 * 30675 61322: contig of 30648 bp in length
 * 61323 61423: gap of unknown length
 * 61423 93101: contig of 31679 bp in length
 * 93102 93201: gap of unknown length
 * 93202 185420: contig of 92219 bp in length.

FEATURES

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1. 185420
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 /db_xref="taxon:9606"
 /chromosome="8"
 /clone="RP11-398H6"

misc_feature

1. 2842
 /note="assembly_name:Contig8
 clone_end:T7
 vector_side:right"

misc_feature

2943..6917
 /note="assembly_name:Contig9"

misc_feature

7018..15680
 /note="assembly_name:Contig10"

misc_feature

15781..30574
 /note="assembly_name:Contig11"

misc_feature

30675..61322
 /note="assembly_name:Contig12"

misc_feature

61423..93101
 /note="assembly_name:Contig13
 clone_end:SP6
 vector_side:left"

misc_feature

93202..185420
 /note="assembly_name:Contig14"

BASE COUNT 53244 a 39520 c 39207 g 52848 t 601 others
 ORIGIN

Query Match 23.7%; Score 43.4; DB 2; Length 185420;
 Best Local Similarity 72.7%; Pred. No. 0.0029;
 Matches 56; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 65 AGAAGGAGAAATGTGGTGGAGCTATTATTCGCCAGTGCCTCCCTGGCGGTATGGAT 124
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 167596 AGAAGCAGAGGAGATCAGGCGCTTTGTTACCAAGTTCCTCCCTCTCTAAGGTT 167537
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 125 GACAGTGGCTGACTTC 141
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 167536 TCACAGTGGCTTTCTTC 167520
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9

AC013751

LOCUS

DEFINITION

AC013751

ACCESSION

VERSION

KEYWORDS

AC013751 AC013751 205816 bp DNA linear PRI 07-MAY-2001
 DEFINITION Homo sapiens chromosome, clone RP11-298P6, complete sequence.
 AC013751
 AC013751.6 GI:13958504
 HTG.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

Homo sapiens.

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 205816)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome, clone RP11-298P6

Unpublished

2 (bases 1 to 205816)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,

Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A.,

Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donegan,L., Doyle,M.,

Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,

Galagan,J., Gardyna,S., Grant,G., Hagos,B., Hearford,A., Horton,L.,

Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,

Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,

McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,

Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,

Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 205816)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,

Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A.,

Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,

Collins,S., Collamore,A., Cooke,P., Dearellano,K., Dewar,K.,

Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Grand-Pierre,N., Hagos,B., Hearford,A., Horton,L., Hulme,W.,

Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRoque,K.,

Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,

Maclean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,

McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,

Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,

Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,

Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,

Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,

Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,

Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,

Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,

Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,

Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,

Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (06-MAY-2001) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 205816)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,

Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A.,

Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,

Collins,S., Collamore,A., Cooke,P., Dearellano,K., Dewar,K.,

Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Grand-Pierre,N., Hagos,B., Hearford,A., Horton,L., Hulme,W.,

Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRoque,K.,

Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,

Maclean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,

McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,

Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,

Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,

Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,

Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,

Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,

Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,

Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,

Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,

Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,

Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

RESULT 10
AC016075
LOCUS
AC016075 174380 bp DNA linear HTG 17-MAR-2000
DEFINITION Homo sapiens clone RP11-699A7, WORKING DRAFT SEQUENCE, 12 unordered
pieces.
ACCESSION
AC016075

AUTHORS

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Usman, F.R., Allen, C., Alsbrooks, S.L., Amaratunga, H.C., Are, J.R., Banks, T., Barbara, J., Banton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovach, S., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegh, H., Lozada, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okuwonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaite, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, F., Wu, F.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 175559)
Worley, K.C.
Direct Submission
Submitted (21-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 175559)
Worley, K.C.
Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 175559)
Worley, K.C.
Direct Submission
Submitted (26-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 175559)
Worley, K.C.
Direct Submission
Submitted (28-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 26, 2002 this sequence version replaced gi:20335921.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones.

Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot.attn.html>.

FEATURES

source

Location/Qualifiers

1. 175559
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/db_xref="taxon:9606"
/chromosome="X"
/clone="RP11-699A7"

repeat_region

1. 2494
/rpt_family="L1M3f"

misc_feature

1. 2004
/note="overlaps bases 123282..125285 of clone AC121340"

repeat_region

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repeat_region

2615..3368
/rpt_family="L1MA8"

repeat_region

3376..3439
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repeat_region

3540..3926
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repeat_region

3958..4105
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repeat_region

4469..4494
/rpt_family="(TTTA)n"

repeat_region

complement(4508..4793)
/rpt_family="AluY"

repeat_region

5704..5739
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repeat_region

complement(5747..6027)
/rpt_family="AluJb"

repeat_region

6062..6199
/rpt_family="MLT1A2"

repeat_region

complement(6217..6367)
/rpt_family="L1MB2"

repeat_region

6854..6888
/rpt_family="(CAAG)n"

repeat_region

6891..6929
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repeat_region

complement(7307..7709)
/rpt_family="LTR16A"

repeat_region

8153..8249
/rpt_family="MIR"

repeat_region

8323..8343
/rpt_family="AT-rich"

repeat_region

8344..8528

Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
 Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
 Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fato, S.,
 Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-pierre, N.,
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kamat, A., Karatas, A., Kellis, C., LaRocque, K., Lamazares, R.,
 Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C.,
 Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
 McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T.,
 Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
 Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
 Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
 Retta, R., Ribback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
 Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
 Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Triglilio, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE JOURNAL

COMMENT

Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 13, 2002 this sequence version replaced gi:18308592.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submission@genome.wi.mit.edu

----- Project Information

Center project name: L22007

Center clone name: 640_C_18

* NOTE: This record contains 73 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

1 679: contig of 679 bp in length
 * 680 779: gap of 100 bp
 * 780 1492: contig of 713 bp in length
 * 1493 1592: gap of 100 bp
 * 1593 2305: contig of 713 bp in length
 * 2306 2405: gap of 100 bp
 * 2406 3042: contig of 637 bp in length
 * 3043 3142: gap of 100 bp
 * 3143 3855: contig of 713 bp in length
 * 3856 3955: gap of 100 bp
 * 3956 4648: contig of 693 bp in length
 * 4649 4748: gap of 100 bp
 * 4749 5465: contig of 717 bp in length
 * 5466 5565: gap of 100 bp
 * 5566 6259: contig of 694 bp in length
 * 6260 6359: gap of 100 bp
 * 6360 7056: contig of 697 bp in length
 * 7057 7156: gap of 100 bp
 * 7157 7810: contig of 654 bp in length
 * 7811 7910: gap of 100 bp
 * 7911 8627: contig of 717 bp in length
 * 8628 8727: gap of 100 bp
 * 8728 9400: contig of 673 bp in length
 * 9401 9500: gap of 100 bp
 * 9501 10214: contig of 714 bp in length
 * 10215 10314: gap of 100 bp

10315 11020: contig of 706 bp in length
 * 11021 11120: gap of 100 bp
 * 11121 11846: contig of 726 bp in length
 * 11847 11946: gap of 100 bp
 * 11947 12661: contig of 715 bp in length
 * 12662 12761: gap of 100 bp
 * 12762 13467: contig of 706 bp in length
 * 13468 13567: gap of 100 bp
 * 13568 14271: contig of 704 bp in length
 * 14272 14371: gap of 100 bp
 * 14372 15069: contig of 698 bp in length
 * 15070 15169: gap of 100 bp
 * 15170 15882: contig of 713 bp in length
 * 15883 15982: gap of 100 bp
 * 15983 16700: contig of 718 bp in length
 * 16701 16800: gap of 100 bp
 * 16801 17501: contig of 701 bp in length
 * 17502 17601: gap of 100 bp
 * 17602 18328: contig of 727 bp in length
 * 18329 18428: gap of 100 bp
 * 18429 19117: contig of 689 bp in length
 * 19118 19217: gap of 100 bp
 * 19218 19925: contig of 708 bp in length
 * 19926 20025: gap of 100 bp
 * 20026 20753: contig of 730 bp in length
 * 20756 20855: gap of 100 bp
 * 20856 21567: contig of 711 bp in length
 * 21567 21666: gap of 100 bp
 * 21667 22374: contig of 708 bp in length
 * 22375 22474: gap of 100 bp
 * 22475 23181: contig of 707 bp in length
 * 23182 23281: gap of 100 bp
 * 23282 24001: contig of 720 bp in length
 * 24002 24101: gap of 100 bp
 * 24102 24811: contig of 710 bp in length
 * 24812 24911: gap of 100 bp
 * 24912 25600: contig of 689 bp in length
 * 25601 25700: gap of 100 bp
 * 25701 28422: contig of 722 bp in length
 * 28423 28522: gap of 100 bp
 * 28523 27228: contig of 706 bp in length
 * 27229 27328: gap of 100 bp
 * 27329 28041: contig of 713 bp in length
 * 28042 28141: gap of 100 bp
 * 28142 28844: contig of 703 bp in length
 * 28845 28944: gap of 100 bp
 * 28945 29628: contig of 684 bp in length
 * 29629 29728: gap of 100 bp
 * 29729 30423: contig of 695 bp in length
 * 30424 30523: gap of 100 bp
 * 30524 31235: contig of 712 bp in length
 * 31236 31335: gap of 100 bp
 * 31336 31979: contig of 644 bp in length
 * 31980 32079: gap of 100 bp
 * 32080 32797: contig of 718 bp in length
 * 32798 32897: gap of 100 bp
 * 32898 33595: contig of 698 bp in length
 * 33596 33695: gap of 100 bp
 * 33696 34416: contig of 721 bp in length
 * 34417 34516: gap of 100 bp
 * 34517 35235: contig of 719 bp in length
 * 35236 35335: gap of 100 bp
 * 35336 36034: contig of 699 bp in length
 * 36035 36134: gap of 100 bp
 * 36135 36846: contig of 712 bp in length
 * 36847 36946: gap of 100 bp
 * 36947 37670: contig of 724 bp in length
 * 37671 37770: gap of 100 bp
 * 37771 38479: contig of 709 bp in length
 * 38480 38579: gap of 100 bp
 * 38580 39287: contig of 708 bp in length
 * 39288 39387: gap of 100 bp
 * 39388 40105: contig of 718 bp in length

*	40106	40205:	gap of	100 bp
*	40206	40918:	contig of 713 bp	in length
*	40919	41018:	gap of	100 bp
*	41019	41723:	contig of 705 bp	in length
*	41724	41823:	gap of	100 bp
*	41824	42495:	contig of 672 bp	in length
*	42496	42595:	gap of	100 bp
*	42596	43285:	contig of 690 bp	in length
*	43286	43385:	gap of	100 bp
*	43386	44095:	contig of 710 bp	in length
*	44096	44195:	gap of	100 bp
*	44196	44894:	contig of 699 bp	in length
*	44895	44994:	gap of	100 bp
*	44995	45705:	contig of 711 bp	in length
*	45706	45805:	gap of	100 bp
*	45806	46517:	contig of 712 bp	in length
*	46518	46617:	gap of	100 bp
*	46618	47326:	contig of 709 bp	in length
*	47327	47426:	gap of	100 bp
*	47427	48155:	contig of 729 bp	in length
*	48156	48255:	gap of	100 bp
*	48256	48985:	contig of 730 bp	in length
*	48986	49085:	gap of	100 bp
*	49086	49803:	contig of 718 bp	in length
*	49804	49903:	gap of	100 bp
*	49904	50623:	contig of 720 bp	in length
*	50624	50723:	gap of	100 bp
*	50724	51432:	contig of 709 bp	in length
*	51433	51532:	gap of	100 bp
*	51533	52248:	contig of 716 bp	in length
*	52249	52348:	gap of	100 bp
*	52349	53068:	contig of 720 bp	in length
*	53069	53168:	gap of	100 bp
*	53169	53881:	contig of 713 bp	in length
*	53882	53981:	gap of	100 bp
*	53982	54683:	contig of 702 bp	in length
*	54684	54783:	gap of	100 bp

Query Match 22.7%; Score 41.6; DB 2; Length 58693;
Best Local Similarity 62.5%; Pred. No. 0.011;
Matches 65; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

RESULT 14	
AP005368/c	
LOCUS	
DEFINITION	Homo sapiens genomic DNA, chromosome 8q23, clone: KB870F5, complete sequence.
ACCESSION	AP005368
VERSION	AP005368.2
KEYWORDS	GI:22004069
SOURCE	Homo sapiens pre-pro-B cell cell_line:FLEB 14 - 14 DNA, clone_lib:Keio BAC library clone:KB870F5.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 Shimizu,N. and Asakawa,S. Homo sapiens DNA chromosome 8 SEQUENCE Published Only in Database (2002) 2 (bases 1 to 111461) Shimizu,N. and Asakawa,S. Direct Submission Submitted (30-MAY-2002) Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo
AUTHORS	
TITLE	
JOURNAL	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L21920
 Center clone name: 91_D_24

TITLE	Submitted (26-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
JOURNAL	Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE	3 (bases 1 to 149126)
Direct Submission	
Accession Number:	U08707; Genbank accession number: U08707

[illegible]

TITLE	Direct Submission
JOURNAL	Submitted (29-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE	4 (bases 1 to 149126)

[illegible]

TITLE
JOURNAL
COMMENT
 zainoun,J., zempek,D., zimner,A. and zooy,M.
 Direct Submission
 Submitted (01-MAY-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 29, 2002 this sequence version replaced gi:20334653.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center

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30346. .30432
repeat_region /rpt_family="L1MA8"
complement(30433. .30755)
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Query Match 22.7%; Score 41.6; DB 9; Length 149126;
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Matches 62; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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DB 81299 AGGCAGGAGGAGAGTGGTCAAGGCTCTCAATTTCTTGTACCTCCCTATTGTGCA 81240

QY 120 TGGATCAACAGTGGTGACTTCATCTAGGAAAGAGC 155
DB 81239 TGAATTATCAGTGTCTTTCTTCTTCTACCAAGGC 81204
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Search completed: May 25, 2003, 03:59:04
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